

This listing of claims will replace all prior versions, and listings of claims in the application  
(Please cancel claims 1-38 and add new claims 39-68):

**Listing of Claims:**

Claims 1-38 (canceled)

Claim 39 (new): A method for identification of a nucleic acid molecule that modulates a process in a biological system comprising the steps of:

- a) introducing a random library of a nucleic acid catalyst into said biological system under conditions suitable for modulating said process, wherein said nucleic acid catalyst comprises a substrate binding domain and a catalytic domain, said substrate binding domain comprises a random sequence; and
- b) determining the nucleotide sequence of at least a portion of the substrate binding domain of said nucleic acid catalyst from said biological system in which the process has been modulated.

Claim 40 (new): A method for identifying one or more nucleic acid molecules involved in a process in a biological system comprising the steps of:

- a) providing a library of a nucleic acid catalyst, with a substrate binding domain and a catalytic domain, wherein said substrate binding domain comprises a random sequence, to said biological system under conditions suitable for said process to be altered;
- b) identifying any said nucleic acid catalyst present in said biological system where said process has been altered; and
- c) determining the nucleotide sequence of at least a portion of the binding domain of said any said nucleic acid catalyst to allow said identification of said nucleic acid molecule involved in said process in said biological system.

Claim 41 (new): A method for identification of a nucleic acid catalyst that modulates a process in a biological system comprising the steps of:

- a) introducing a random library of a nucleic acid catalyst into said biological system under conditions suitable for modulating said process, wherein said nucleic acid catalyst comprises a substrate binding domain and a catalytic domain, said substrate binding domain comprises a random sequence; and
- b) identifying said nucleic acid catalyst from said biological system in which the process has been modulated.

Claim 42 (new): The method of any of claims 39-41, wherein said biological system is a bacterial cell.

Claim 43 (new): The method of any of claims 39-41, wherein said biological system is of plant origin.

Claim 44 (new): The method of any of claims 39-41, wherein said biological system is of mammalian origin.

Claim 45 (new): The method of any of claims 39-41, wherein said nucleic acid catalyst is in a hammerhead motif.

Claim 46 (new): The method of any of claims 39-41, wherein said nucleic acid catalyst is in a hairpin motif.

Claim 47 (new): The method of any of claims 39-41, wherein said nucleic acid catalyst is in a group I intron ribozyme motif, group II intron ribozyme motif, VS ribozyme motif or RNase P ribozyme motif.

Claim 48 (new): The method of any of claims 39-41, wherein said process is selected from the group consisting of growth, proliferation, apoptosis, morphology, angiogenesis,

differentiation, migration, viral multiplication, drug resistance, signal transduction, cell cycle regulation, temperature sensitivity and chemical sensitivity.

Claim 49 (new): The method of any of claims 39-41, wherein said random library of nucleic acid catalysts is encoded by an expression vector in a manner which allows expression of said nucleic acid catalysts.

Claim 50 (new): The method of claim 49, wherein said expression vector comprises:

- a) a transcription initiation region;
- b) a transcription termination region;
- c) a sequence encoding at least one said nucleic acid catalyst; and

wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 51 (new): The method of claim 49, wherein said expression vector comprises:

- a) a transcription initiation region;
- b) a transcription termination region;
- c) an open reading frame for a polypeptide;
- d) a sequence encoding at least one said nucleic acid catalyst,

wherein said sequence is operably linked to the 3'-end of said open reading frame;

and

wherein said sequence is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression or delivery or expression and delivery of said nucleic acid catalyst.

Claim 52 (new): The method of claim 49, wherein said expression vector comprises:

- a) a transcription initiation region;
- b) a transcription termination region;

c) an intron;  
d) a sequence encoding at least one said nucleic acid catalyst; and  
wherein said sequence is operably linked to said initiation region, said intron and  
said termination region, in a manner which allows expression or delivery or expression and  
delivery of said nucleic acid catalyst.

Claim 53 (new): The method of claim 49, wherein said expression vector comprises:

a) a transcription initiation region;  
b) a transcription termination region;  
c) an intron;  
d) an open reading frame for a polypeptide;  
e) a sequence encoding at least one said nucleic acid catalyst,  
wherein said sequence is operably linked to the 3'-end of said open reading frame;

and

wherein said sequence is operably linked to said initiation region, said intron, said  
open reading frame and said termination region, in a manner which allows expression or delivery  
or expression and delivery of said nucleic acid catalyst.

Claim 54 (new): The method of claim 49, wherein said expression vector is derived from  
a retrovirus.

Claim 55 (new): The method of claim 49, wherein said expression vector is derived from  
an adenovirus.

Claim 56 (new): The method of claim 49, wherein said expression vector is derived from  
an adeno-associated virus.

Claim 57 (new): The method of claim 49, wherein said expression vector is derived from  
an alphavirus.

Claim 58 (new): The method of claim 49, wherein said expression vector is derived from a bacterial plasmid.

Claim 59 (new): The method of claim 49, wherein said expression vector is operably linked to a RNA polymerase II promoter element.

Claim 60 (new): The method of claim 49, wherein said expression vector is operably linked to a RNA polymerase III promoter element.

Claim 61 (new): The method of claim 49, wherein said RNA polymerase III promoter is derived from a transfer RNA gene.

Claim 62 (new): The method of any of claims 39-41, wherein said biological system is of an eukaryotic origin.

Claim 63 (new): The method of any of claims 39-41, wherein said biological system is of a prokaryotic origin.

Claim 64 (new): The method of any of claims 39-41, wherein said substrate binding domain is of length between 12 and 100 nucleotides.

Claim 65 (new): The method of any of claims 39-41, wherein said substrate binding domain is of length between 14 and 24 nucleotides.

Claim 66 (new): The method of any of claims 39-41, wherein said nucleic acid catalyst comprises two substrate binding arms.

Appl. No.  
Amdt. dated July 2, 2003  
Preliminary Amendment

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Claim 67 (new): The method of claim 66, wherein said substrate binding arms are of similar length.

Claim 68 (new): The method of claim 66, wherein said substrate binding arms are of different length.--